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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/676,380A

DATE: 04/20/2001

TIME: 07:49:17

Input Set : A:\ES.txt

Output Set: N:\CRF3\04202001\I676380A.raw

ENTERED

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2 <110> APPLICANT: Maihle, Nita Reiter, Jill Baron, Andre
W--> 3 <120> TITLE OF INVENTION: SOLUBLE EPIDERMAL GROWTH FACTOR RECEPTOR-LIKE PROTEINS AND THEIR USES
IN
W--> 4      CANCER DETECTION METHODS
W--> 5 <130> FILE REFERENCE: TBIG
C--> 6 <140> CURRENT APPLICATION NUMBER: US/09/676,380A
C--> 6 <141> CURRENT FILING DATE: 2000-09-29
W--> 6 <160> NUMBER OF SEQ ID: 20
7 <170> SOFTWARE: PatentIn version 3.0
W--> 8 <210> SEQ ID NO: 1
9 <211> LENGTH: 705
10 <212> TYPE: PRT
11 <213> ORGANISM: homo sapiens
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18      20      25      30
20 Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
21      35      40      45
23 Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
24      50      55      60
26 Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
27 65      70      75      80
29 Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
30      85      90      95
32 Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
33      100     105     110
35 Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
36      115     120     125
38 Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
39      130     135     140
41 His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
42 145     150     155     160
44 Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
45      165     170     175
47 Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
48      180     185     190
50 Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
51      195     200     205
53 Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
54      210     215     220
56 Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
57 225     230     235     240
59 Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
60      245     250     255
62 Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
63      260     265     270

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65 Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
66      275      280      285
68 Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
69      290      295      300
71 Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
72 305      310      315      320
74 Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
75      325      330      335
77 Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
78      340      345      350
80 Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
81      355      360      365
83 Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
84      370      375      380
86 Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
87 385      390      395      400
89 Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
90      405      410      415
92 Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
93      420      425      430
95 His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
96      435      440      445
98 Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
99      450      455      460
101 Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
102 465      470      475      480
104 Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
105      485      490      495
107 Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
108      500      505      510
110 Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
111      515      520      525
113 Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Lys Leu Leu Glu Gly
114      530      535      540
116 Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
117 545      550      555      560
119 Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
120      565      570      575
122 Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
123      580      585      590
125 Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
126      595      600      605
128 Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
129      610      615      620
131 Thr Tyr Gly Pro Gly Asn Glu Ser Leu Lys Ala Met Leu Phe Cys Leu
132 625      630      635      640
134 Phe Lys Leu Ser Ser Cys Asn Gln Ser Asn Asp Gly Ser Val Ser His
135      645      650      655
137 Gln Ser Gly Ser Pro Ala Ala Gln Glu Ser Cys Leu Gly Trp Ile Pro

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Input Set : A:\ES.txt

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138 660 665 670
 140 Ser Leu Leu Pro Ser Glu Phe Gln Leu Gly Trp Gly Gly Cys Ser His
 141 675 680 685
 143 Leu His Ala Trp Pro Ser Ala Ser Val Ile Ile Thr Ala Ser Ser Cys
 144 690 695 700
 146 His
 147 705

149 <210> SEQ ID NO: 2

150 <211> LENGTH: 2850

151 <212> TYPE: DNA

152 <213> ORGANISM: homo sapiens

W--> 153 <400> SEQUENCE: 2

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156 ccgaggcgccg cggagtcgcc agctagcccc ggcgcccgcc gccgcccaga ccggacgaca 120
158 ggcacacctcg tcggcgctccg cccgagtcgcc cgcctcgccg ccaacgccac aaccaccgcg 180
160 cacggccccc tgactccgtc cagtattgat cgggagagcc ggagcgagct cttcggggag 240
162 cagcgatgcg accctccggg acggccgggg cagcgctcct ggcgctgctg gctgcgctct 300
164 gccggcgagc tcgggctctg gagggaaaaga aagtttgcca aggcacgagt aacaagctca 360
166 cgcagttggg cacttttgaa gatcattttc tcagcctcca gaggatgttc aataactgtg 420
168 agtggtcctc tgggaatttg gaaattacct atgtgcagag gaattatgat ctttcttct 480
170 taaagaccat ccaggaggtg gctggttatg tcctcattgc cctcaacaca gtggagcgaa 540
172 ttccctttgga aaacctgcag atcatcagag gaaatatgta ctacgaaaat tcctatgcct 600
174 tagcagtcct atctaactat gatgcaata aaaccggact gaaggagctg cccatgagaa 660
176 atttacagga aatcctgcac ggcgccgtgc ggttcagcaa caaccatgcc ctgtgcaatg 720
178 tggagagcat ccagtggcggg gacatagtcg gcagtgactt tctcagcaac atgtcgatgg 780
180 acttcagaa ccacctgggc agctgccaaa agtgtgatcc aagctgtccc aatgggagct 840
182 gctgggggtc aggagaggag aactgccaga aactgaccaa aatcatctgt gccagcagt 900
184 gtcgggggag ctgccgtggc aagtcccca gtgactgctg ccacaaccag tgtgctgcag 960
186 gctgcacagg ccccggggag agcgactgcc tggctgcgg caaattccga gacgaagcca 1020
188 cgtgcaagga cacctgcccc ccactcatgc tctacaaccc caccagtcac cagatggatg 1080
190 tgaaccccgga gggcaaatat agctttgtgt ccacctgcgt gaagaagtgt ccccgtaatt 1140
192 atgtggtgac agatcacggc tcgtgcgtcc gagcctgtgg ggccgacagc tatgagatgg 1200
194 aggaagacgg cgtccgcaag tgtaagaagt gcgaagggcc ttgccgaaa gtgtgtaacg 1260
196 gaataggtat tgggtgaattt aaagactcac tctccataaa tgctacgaat attaaacact 1320
198 tcaaaaactg cacctccatc agtggcgatc tccacatcct gccggtggca tttaggggtg 1380
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204 cctttgagaa cctagaaatc atacgcggca ggaccaagca acatggtcag ttttctcttg 1560
206 cagtcgtcag cctgaacata acatccttgg gattacgtc cctcaaggag ataagtgatg 1620
208 gagatgtgat aatttcagga aacaaaaatt tgtgctatgc aaatacaata aactggaaaa 1680
210 aactgttttg gacctccggt cagaaaacca aaattataag caacagaggt gaaaacagct 1740
212 gcaaggccac aggccaggtc tgccatgcct tgtgtcccc cgagggtgc tggggcccg 1800
214 agcccaggga ctgctctct tgccggaatg tcagccgagg cagggaatgc gtggacaagt 1860
216 gcaagcttct ggagggtgag ccaaggaggt ttgtggagaa ctctgagtcg atacagtgc 1920
218 acccagagtg cctgcctcag gccatgaaca tcacctgcac aggcagggga ccagacaact 1980
220 gtatccagtg tgcccactac attgacggcc cccactgcgt caagacctgc ccggcaggag 2040
222 tcatgggaga aaacaacacc ctggtctgga agtacgcaga cgcggccat gtgtgccacc 2100
224 tgtgccatcc aaactgcacc tacgggccag gaaatgagag tctcaaagcc atgttattct 2160
226 gcctttttta actatcatcc tgtaatcaaa gtaatgatgg cagcgtgtcc caccagagcg 2220

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228 ggagcccagc tgcacaggag tcatgcttag gatggatccc ttctcttctg ccgtcagagt 2280
230 ttcagctggg ttgggggtga tgcagccacc tccatgcctg gccttctgca tctgtgatca 2340
232 tcacggcctc ctcttgccac tgagcctcat gccttcacgt gtctgttccc cccacttttc 2400
234 ctttctgcca cccctgcacg tgggcccgcc gggtccaaga gtatcctacc catttccttc 2460
236 ctccaactcc ctttgccagt gcctctcacc ccaactagta gctaaccatc acccccagga 2520
238 ctgacctctt cctcctcgct gccagatgat tgttcaaagc acagaatttg tcagaaacct 2580
240 gcagggagcg catgctgcca gccttctccg taattagcat ggccccagtc catgcttcta 2640
242 gccttggttc cttctgcccc tctgtttgaa attctagagc cagctgtggg acaattatct 2700
244 gtgtcaaaag ccagatgtga aaacatctca ataacaaact ggctgctttg ttcaatgcta 2760
246 gaacaacgcc tgtcacagag tagaaactca aaaatatattg ctgagtgaat gaacaaatga 2820
248 ataatagcat aataaataat taaccaccaa 2850

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251 <210> SEQ ID NO: 3

252 <211> LENGTH: 641

253 <212> TYPE: PRT

254 <213> ORGANISM: homo sapiens

W--> 255 <400> SEQUENCE: 3

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261 20 25 30
263 Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
264 35 40 45
266 Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
267 50 55 60
269 Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
270 65 70 75 80
272 Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
273 85 90 95
275 Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
276 100 105 110
278 Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
279 115 120 125
281 Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
282 130 135 140
284 His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
285 145 150 155 160
287 Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
288 165 170 175
290 Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
291 180 185 190
293 Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
294 195 200 205
296 Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
297 210 215 220
299 Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
300 225 230 235 240
302 Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
303 245 250 255
305 Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro

```

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TIME: 07:49:17

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Output Set: N:\CRF3\04202001\I676380A.raw

```

306          260          265          270
308 Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
309          275          280          285
311 Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
312          290          295          300
314 Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
315 305          310          315          320
317 Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
318          325          330          335
320 Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
321          340          345          350
323 Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
324          355          360          365
326 Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
327          370          375          380
329 Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
330 385          390          395          400
332 Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
333          405          410          415
335 Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
336          420          425          430
338 His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
339          435          440          445
341 Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
342          450          455          460
344 Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
345 465          470          475          480
347 Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
348          485          490          495
350 Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
351          500          505          510
353 Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
354          515          520          525
356 Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Lys Leu Leu Glu Gly
357          530          535          540
359 Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
360 545          550          555          560
362 Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
363          565          570          575
365 Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
366          580          585          590
368 Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
369          595          600          605
371 Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
372          610          615          620
374 Thr Tyr Gly Pro Gly Asn Glu Ser Leu Lys Ala Met Leu Phe Cys Leu
375 625          630          635          640
377 Phe
380 <210> SEQ ID NO: 4

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VERIFICATION SUMMARY

DATE: 04/20/2001

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TIME: 07:49:18

Input Set : A:\ES.txt

Output Set: N:\CRF3\04202001\I676380A.raw

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L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:270 C: Current Application Number differs, Replaced Current Application No
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:6 M:283 W: Missing Blank Line separator, <160> field identifier
L:8 M:283 W: Missing Blank Line separator, <210> field identifier
L:12 M:283 W: Missing Blank Line separator, <400> field identifier
L:153 M:283 W: Missing Blank Line separator, <400> field identifier
L:255 M:283 W: Missing Blank Line separator, <400> field identifier
L:384 M:283 W: Missing Blank Line separator, <400> field identifier
L:525 M:283 W: Missing Blank Line separator, <400> field identifier
L:666 M:283 W: Missing Blank Line separator, <400> field identifier
L:807 M:283 W: Missing Blank Line separator, <400> field identifier
L:815 M:283 W: Missing Blank Line separator, <400> field identifier
L:823 M:283 W: Missing Blank Line separator, <400> field identifier
L:831 M:283 W: Missing Blank Line separator, <400> field identifier
L:839 M:283 W: Missing Blank Line separator, <400> field identifier
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